

Snx14 Cas9-CKO Strategy

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Overview

Target Gene Name

- Snx14

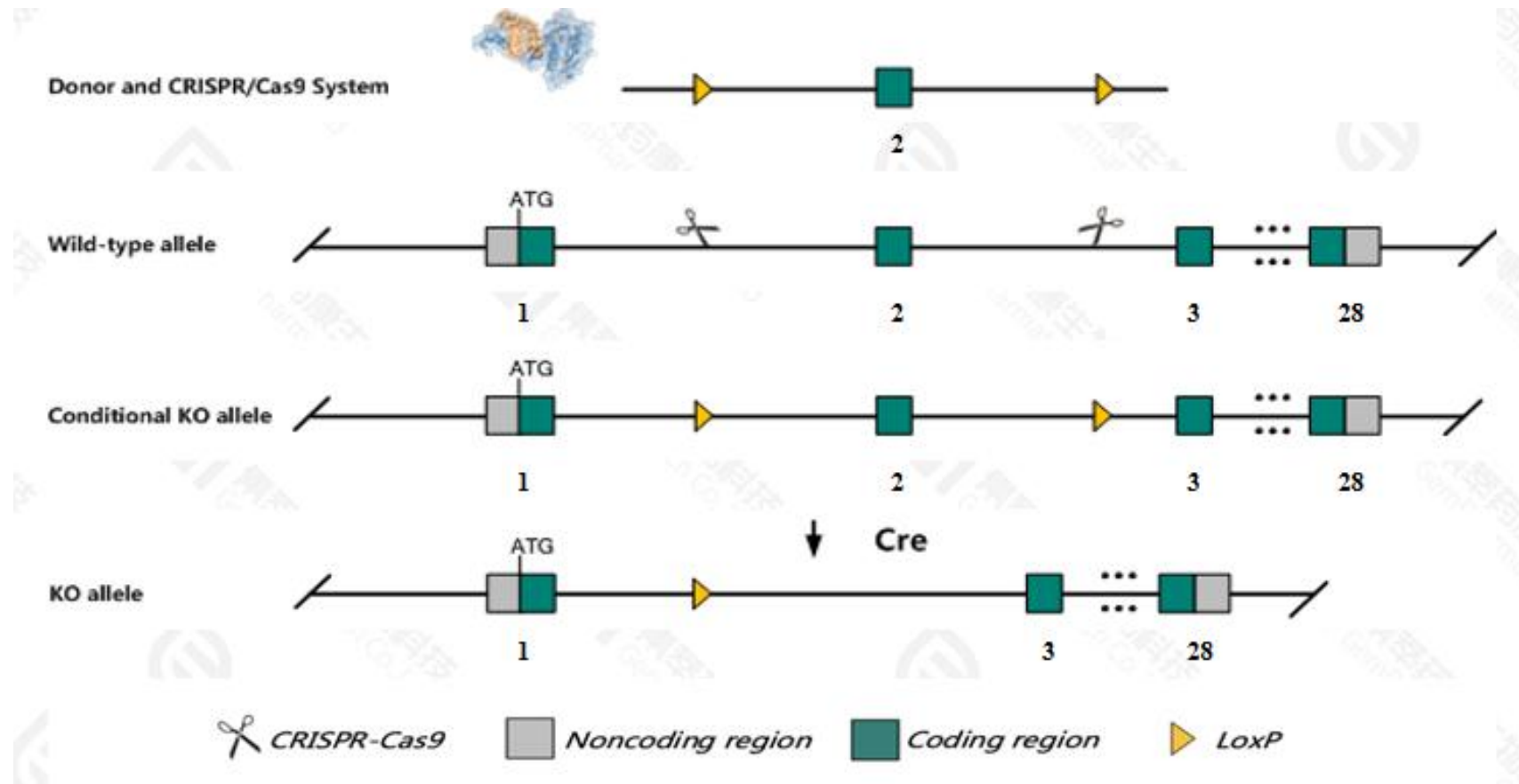
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Snx14* gene.

Technical Information

- The *Snx14* gene has 9 transcripts. According to the structure of *Snx14* gene, , exon2 of *Snx14-209*(ENSMUST00000239462.2) transcript is recommended as the knockout region. The region contains 121bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Snx14* gene. The brief process is as follows: CRISPR-Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

Snx14 sorting nexin 14 [*Mus musculus* (house mouse)]

Gene ID: 244962, updated on 5-Jan-2023

[Download Datasets](#)

Summary

Official Symbol	Snx14 provided by MGI
Official Full Name	sorting nexin 14 provided by MGI
Primary source	MGI:MGI:2155664
See related	Ensembl:ENSMUSG00000032422 AllianceGenome:MGI:2155664
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	YR-14; B830022K16; C330035N22Rik
Summary	Predicted to enable phosphatidylinositol-3,5-bisphosphate binding activity. Predicted to be involved in autophagosome maturation. Predicted to act upstream of or within protein transport. Predicted to be located in cytosol and lysosome. Predicted to be active in late endosome. Human ortholog(s) of this gene implicated in autosomal recessive spinocerebellar ataxia 20. Orthologous to human SNX14 (sorting nexin 14). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in bladder adult (RPKM 4.9), CNS E18 (RPKM 4.5) and 28 other tissues See more
Orthologs	human all
NEW	Try the new Gene table Try the new Transcript table

Genomic context

Location: 9; 9 E3.1

Exon count: 30

See Snx14 in [Genome Data Viewer](#)

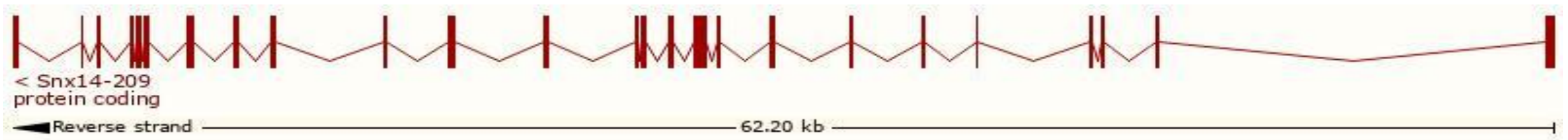
Source: <https://www.ncbi.nlm.nih.gov/>

Transcript Information

The gene has 9 transcripts, all transcripts are shown below:

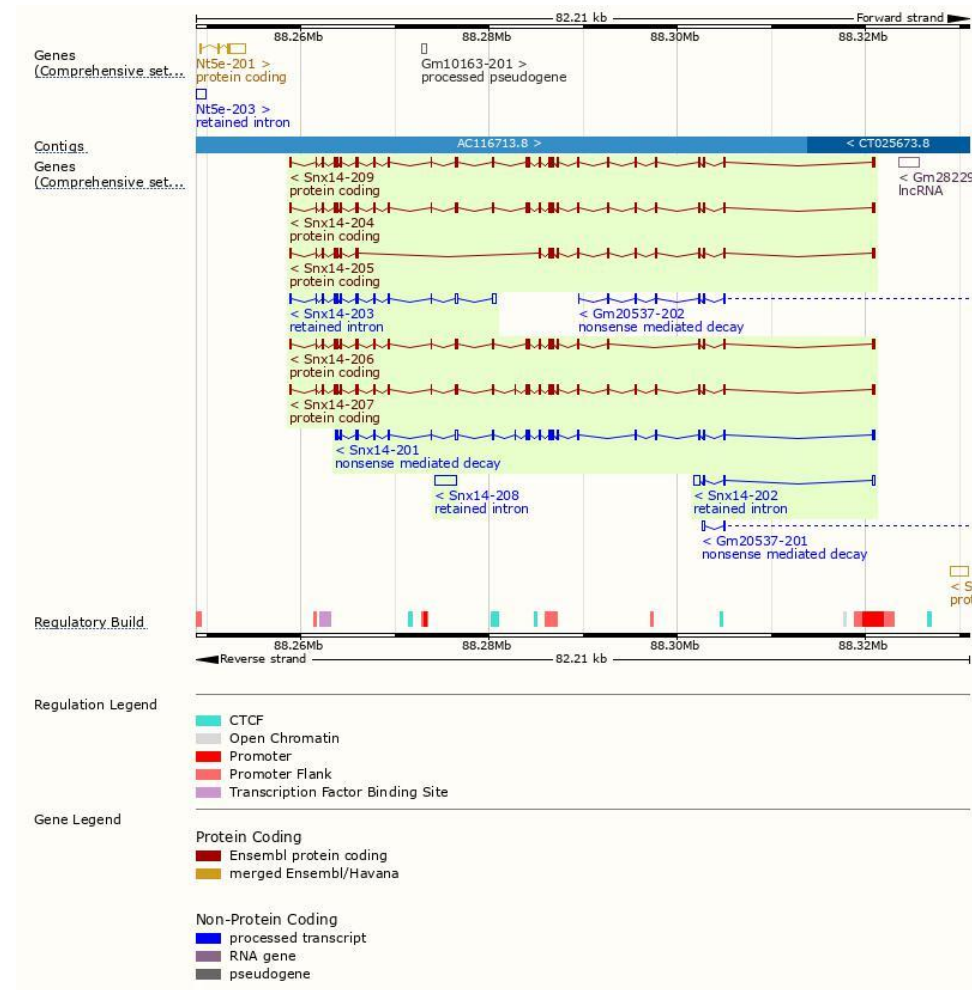
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000239462.2	Snx14-209	3112	964aa	Protein coding	CCDS23387	Q8BHY8	Ensembl Canonical Gencode basic
ENSMUST00000165315.9	Snx14-204	3109	937aa	Protein coding		A0A6Q6RCM4	Gencode basic APPRIS P4 TSL:1
ENSMUST00000174806.9	Snx14-207	3082	946aa	Protein coding		G3UX33	Gencode basic APPRIS ALT1 TSL:5
ENSMUST00000173039.9	Snx14-206	2970	893aa	Protein coding		G3UXB6	Gencode basic TSL:5
ENSMUST00000173011.9	Snx14-205	2238	665aa	Protein coding		G3UX13	Gencode basic TSL:5
ENSMUST00000126405.3	Snx14-201	2633	183aa	Nonsense mediated decay		D6RH84	TSL:1
ENSMUST00000187610.2	Snx14-208	2269	No protein	Retained intron		-	TSL:NA
ENSMUST00000140439.8	Snx14-203	1765	No protein	Retained intron		-	TSL:1
ENSMUST00000126563.3	Snx14-202	1075	No protein	Retained intron		-	TSL:2

The strategy is based on the design of *Snx14-209* transcript, the transcription is shown below:

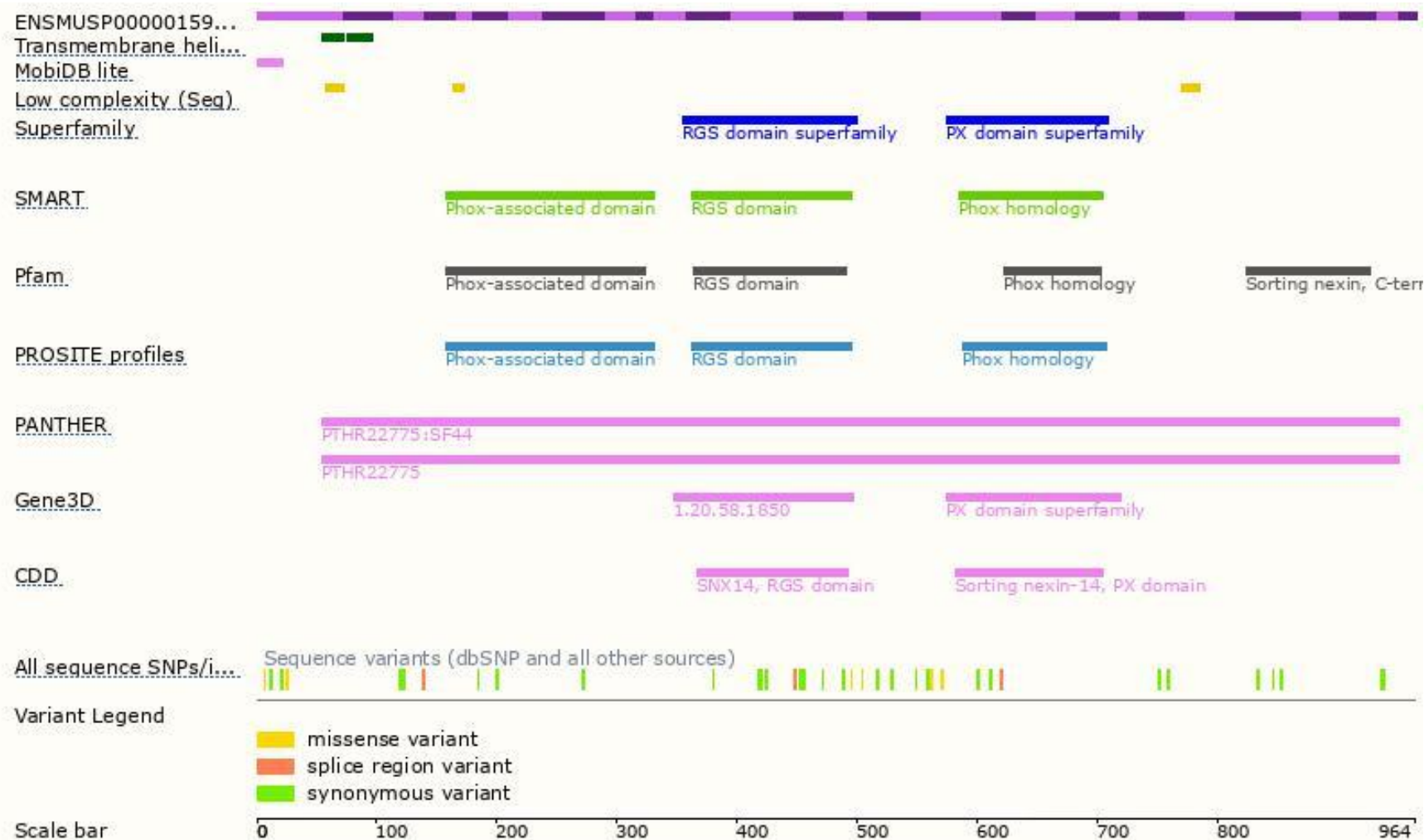


Source: <https://www.ensembl.org>

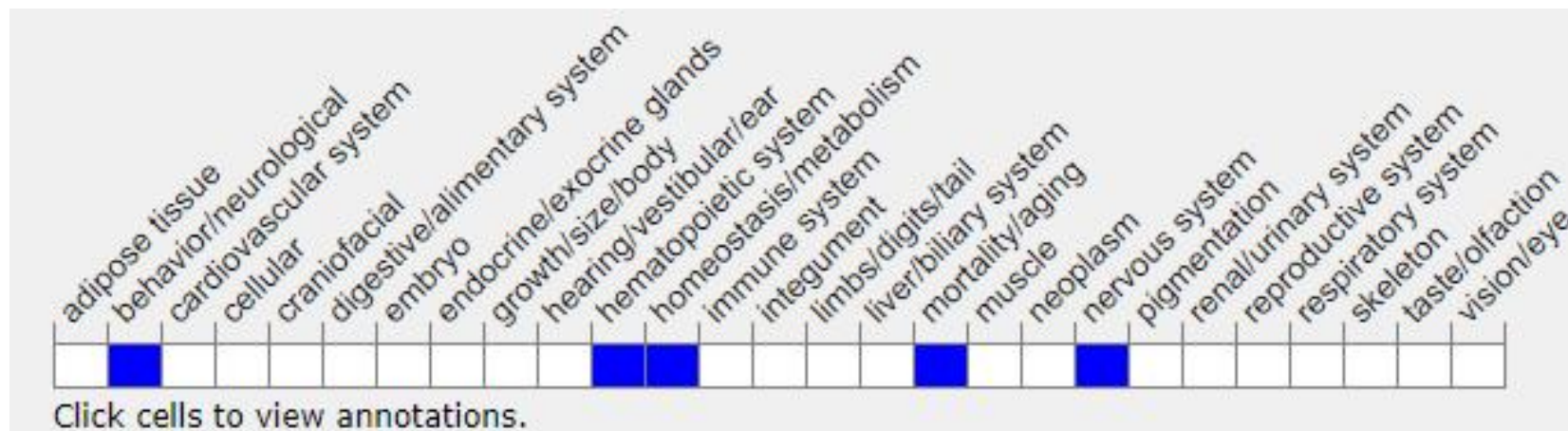
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Phenotypes affected by the gene are marked in blue. Data quoted from MGI database (<http://www.informatics.jax.org/>).

Important Information

- *Gm20537* gene will be destroyed.
- The *Snx14* gene is located on the Chr9. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.